

**SCORE Search Results for Application 10025222**[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you a list of all the Search Results. Use this page to obtain specific Search Result information.

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Item Name	Download Content
<a href="#">us-10-025-222a-2.oli.rnpb</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rpr</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rsp</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rspt</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rst</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rag</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rai</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rapb</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rge</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rng</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rni</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rnpb</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rpr</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rsp</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rspt</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.std.rst</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rag</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rai</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rapb</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rge</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rng</a>	<a href="#">Download</a>
<a href="#">us-10-025-222a-2.oli.rni</a>	<a href="#">Download</a>

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 03:33:47 ; Search time 2554 Seconds  
(without alignments)  
766.505 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 599  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYLLQIVAKNKERM 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2169961 seqs, 1634102185 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4333168

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141825\_27374/app\_query.fasta\_1  
.775

-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=oli.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10025222\_@CGN\_1\_1\_107\_@runat\_13112003\_141825\_27374  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

```

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	599	100.0	1800	14	US-10-025-222A-1	Sequence 1, Appli
2	290	48.4	1719	15	US-10-282-287-11	Sequence 11, Appl
3	210	35.1	752	8	US-08-781-986A-702	Sequence 702, App
4	149	24.9	782	8	US-08-781-986A-697	Sequence 697, App
5	39	6.5	120	14	US-10-025-222A-5	Sequence 5, Appli
6	12	2.0	1206	10	US-09-974-300-5943	Sequence 5943, Ap
7	10	1.7	1701	10	US-09-974-300-1542	Sequence 1542, Ap
8	9	1.5	403	10	US-09-764-877-486	Sequence 486, App
c 9	9	1.5	936	10	US-09-886-055-470	Sequence 470, App
c 10	9	1.5	936	11	US-09-804-291-470	Sequence 470, App
c 11	9	1.5	1336	12	US-10-017-161-161	Sequence 161, App
12	9	1.5	1359	11	US-09-934-455-515	Sequence 515, App
13	9	1.5	1896	14	US-10-156-761-5658	Sequence 5658, Ap
14	9	1.5	7947	10	US-09-070-927A-84	Sequence 84, Appl
c 15	9	1.5	640681	10	US-09-790-988-1	Sequence 1, Appli
16	9	1.5	1830121	14	US-10-329-960-1	Sequence 1, Appli
17	9	1.5	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 18	8	1.3	26	14	US-10-025-222A-13	Sequence 13, Appl
c 19	8	1.3	28	14	US-10-025-222A-14	Sequence 14, Appl
c 20	8	1.3	213	10	US-09-764-877-2877	Sequence 2877, Ap
21	8	1.3	325	8	US-08-781-986A-2164	Sequence 2164, Ap
22	8	1.3	342	13	US-10-044-090-87	Sequence 87, Appl
c 23	8	1.3	381	8	US-08-781-986A-3857	Sequence 3857, Ap
24	8	1.3	464	10	US-09-867-701-4395	Sequence 4395, Ap
25	8	1.3	471	12	US-10-027-632-56607	Sequence 56607, A
26	8	1.3	471	13	US-10-027-632-56607	Sequence 56607, A
27	8	1.3	522	12	US-10-027-632-3561	Sequence 3561, Ap
28	8	1.3	522	13	US-10-027-632-3561	Sequence 3561, Ap
29	8	1.3	569	12	US-10-027-632-39837	Sequence 39837, A
30	8	1.3	569	13	US-10-027-632-39837	Sequence 39837, A
c 31	8	1.3	571	12	US-10-029-386-8548	Sequence 8548, Ap
32	8	1.3	598	12	US-10-027-632-227475	Sequence 227475,
33	8	1.3	598	13	US-10-027-632-227475	Sequence 227475,
34	8	1.3	606	12	US-10-027-632-3741	Sequence 3741, Ap
35	8	1.3	606	13	US-10-027-632-3741	Sequence 3741, Ap
36	8	1.3	662	9	US-09-815-242-2144	Sequence 2144, Ap
37	8	1.3	663	12	US-10-027-632-198454	Sequence 198454,
38	8	1.3	663	12	US-10-027-632-198455	Sequence 198455,
39	8	1.3	663	13	US-10-027-632-198454	Sequence 198454,
40	8	1.3	663	13	US-10-027-632-198455	Sequence 198455,

c	41	8	1.3	781	12	US-10-027-632-126138	Sequence 126138,
c	42	8	1.3	781	12	US-10-027-632-126139	Sequence 126139,
c	43	8	1.3	781	13	US-10-027-632-126138	Sequence 126138,
c	44	8	1.3	781	13	US-10-027-632-126139	Sequence 126139,
	45	8	1.3	904	12	US-10-027-632-32966	Sequence 32966, A

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:22:09 ; Search time 20 Seconds  
(without alignments)  
2880.252 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 599  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	323	53.9	605	2	A89937 DNA primase [impor
2	12	2.0	626	2	AC1619 DNA primase [impor
3	11	1.8	595	2	F71471 probable DNA prima
4	11	1.8	599	2	G83821 DNA primase dnaG [
5	11	1.8	600	2	H81733 DNA primase TC0175
6	11	1.8	635	2	S75668 DNA primase (EC 2.
7	10	1.7	565	2	H72253 DNA primase - Ther
8	10	1.7	616	2	T11850 DNA primase (EC 2.
9	10	1.7	626	2	AG1256 DNA primase [impor
10	10	1.7	664	2	E83572 DNA primase PA0577
11	9	1.5	399	1	HMXRH2 sigma 1 protein -
12	9	1.5	462	2	C34829 sigma 1 protein -
13	9	1.5	577	2	G82806 DNA primase XF0430
14	9	1.5	577	2	C84936 DNA primase [impor
15	9	1.5	581	1	RYEC2 DNA primase (EC 2.
16	9	1.5	581	1	RYEBT DNA primase (EC 2.
17	9	1.5	581	2	D85967 DNA biosynthesis,
18	9	1.5	581	2	E91122 DNA primase [impor

19	9	1.5	581	2	AI0892	DNA primase [impor
20	9	1.5	582	2	AG0079	DNA primase (EC 2.
21	9	1.5	593	2	A64075	DNA primase (EC 2.
22	9	1.5	595	2	B97866	DNA primase (EC 2.
23	9	1.5	596	2	I40609	DNA primase (EC 2.
24	9	1.5	596	2	C97060	DNA primase, DNAG
25	9	1.5	616	2	C71648	DNA primase (EC 2.
26	9	1.5	637	2	H86693	DNA primase (EC 2.
27	9	1.5	640	2	AH1971	DNA primase [impor
28	9	1.5	642	2	JC2485	DNA primase (EC 2.
29	8	1.3	177	2	H86710	hypothetical prote
30	8	1.3	295	2	E97329	sugar kinase, ribo
31	8	1.3	342	2	C86811	hypothetical prote
32	8	1.3	350	2	A82798	hypothetical prote
33	8	1.3	523	2	E70188	DNA primase (dnaG)
34	8	1.3	680	2	T25146	hypothetical prote
35	8	1.3	681	2	AD3318	DNA primase (EC 2.
36	8	1.3	1159	1	H64089	DNA-directed DNA p
37	7	1.2	49	2	AG0886	conserved hypothet
38	7	1.2	77	2	F69219	conserved hypothet
39	7	1.2	91	2	B69811	conserved hypothet
40	7	1.2	101	2	F82797	hypothetical prote
41	7	1.2	129	2	T20081	hypothetical prote
42	7	1.2	158	2	D90391	conserved hypothet
43	7	1.2	167	2	C86241	protein T16B5.9 [i
44	7	1.2	169	2	A64776	probable membrane
45	7	1.2	169	2	G90692	probable membrane

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:20:19 ; Search time 17 Seconds  
(without alignments)  
1657.000 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 599  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	290	48.4	572	1	PRIM_STAAU	O05338 staphylococ
2	13	2.2	636	1	PRIM_MYCSM	O52200 mycobacteri
3	12	2.0	626	1	PRIM_LISIN	Q92bq5 listeria in
4	11	1.8	595	1	PRIM_CHLTR	O84799 chlamydia t
5	11	1.8	599	1	PRIM_BACHD	Q9kd44 bacillus ha
6	11	1.8	600	1	PRIM_CHLMU	Q9plc9 chlamydia m
7	11	1.8	635	1	PRIM_SYNY3	P74143 synechocyst
8	10	1.7	565	1	PRIM_THEMA	Q9xlg3 thermotoga
9	10	1.7	616	1	PRIM_SYNP7	P74893 synechococc
10	10	1.7	626	1	PRIM_LISMO	P47762 listeria mo
11	10	1.7	660	1	PRIM_PSEPK	O33470 pseudomonas
12	10	1.7	664	1	PRIM_PSEAE	Q9i5w0 pseudomonas
13	9	1.5	462	1	VSI1_REOVJ	P04507 reovirus (t
14	9	1.5	576	1	PRIM_LEGPN	P71481 legionella
15	9	1.5	577	1	PRIM_BUCAI	P57164 buchnera ap
16	9	1.5	581	1	PRIM_ECOLI	P02923 escherichia
17	9	1.5	581	1	PRIM_SALTY	P07362 salmonella
18	9	1.5	582	1	PRIM_PASMU	Q9cli9 pasteurella
19	9	1.5	593	1	PRIM_HAEIN	Q08346 haemophilus
20	9	1.5	593	1	PRIM_RICPR	P30103 rickettsia
21	9	1.5	596	1	PRIM_CLOAB	P33655 clostridium
22	9	1.5	597	1	PRIM_BACST	Q9x4d0 bacillus st

23	9	1.5	628	1	PRIM_ENTFA	P52308	enterococcu
24	9	1.5	637	1	PRIM_LACLA	Q04505	lactococcus
25	9	1.5	641	1	PRIM_STRCO	Q9s1n4	streptomyce
26	8	1.3	254	1	HIS6_THEET	Q9rpq4	thermoanaer
27	8	1.3	523	1	PRIM_BORBU	O51653	borrelia bu
28	8	1.3	578	1	PRIM_BUCBP	Q89b09	buchnera ap
29	8	1.3	579	1	PRIM_BUCAP	P32000	buchnera ap
30	8	1.3	1159	1	DP3A_HAEIN	P43743	haemophilus
31	7	1.2	91	1	ACYP_BACSU	O35031	bacillus su
32	7	1.2	98	1	GROG_BOVIN	O46675	bos taurus
33	7	1.2	103	1	GRO_SHEEP	O46678	ovis aries
34	7	1.2	119	1	RNPA_PASMU	P57915	pasteurella
35	7	1.2	143	1	FUR_ALCEU	O30330	alcaligenes
36	7	1.2	169	1	YLAC_ECOLI	P77523	escherichia
37	7	1.2	170	1	P25B_HUMAN	P59282	homo sapien
38	7	1.2	216	1	DAPB_THEMA	Q9x1k8	thermotoga
39	7	1.2	241	1	HIS4_BIFLO	Q8g4s5	bifidobacte
40	7	1.2	262	1	LAT_HUMAN	O43561	homo sapien
41	7	1.2	262	1	MOAF_KLEAE	P54796	klebsiella
42	7	1.2	305	1	GP7D_CHLMU	Q46435	chlamydia m
43	7	1.2	305	1	GP7D_CHLTR	P10561	chlamydia t
44	7	1.2	309	1	MRAW_WIGBR	Q8d2y8	wiggleswort
45	7	1.2	328	1	YJ77_YEAST	P47145	saccharomyc



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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:21:14 ; Search time 39 Seconds  
(without alignments)  
3963.423 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 599  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	323	53.9	605	16	Q99TT4	Q99tt4 staphylococ
2	200	33.4	605	16	Q8NWB7	Q8nwb7 staphylococ
3	64	10.7	598	16	Q8CP23	Q8cp23 staphylococ
4	13	2.2	694	16	Q8DJB0	Q8djb0 synechococc
5	12	2.0	574	16	Q8EHD9	Q8ehd9 shewanella

6	12	2.0	587	16	Q8DEG2	Q8deg2 vibrio vuln
7	12	2.0	643	2	Q8GDP9	Q8gdp9 heliobacill
8	11	1.8	603	16	Q8XXA0	Q8xxa0 ralstonia s
9	10	1.7	628	2	Q9EZB7	Q9ezb7 zymomonas m
10	10	1.7	702	16	Q8G573	Q8g573 bifidobacte
11	9	1.5	452	10	Q9FK90	Q9fk90 arabidopsis
12	9	1.5	454	12	Q86339	Q86339 reovirus sp
13	9	1.5	454	12	Q86340	Q86340 reovirus sp
14	9	1.5	462	12	Q85663	Q85663 reovirus (t
15	9	1.5	465	10	Q9FHT1	Q9fht1 arabidopsis
16	9	1.5	493	10	Q8LE46	Q8le46 arabidopsis
17	9	1.5	577	16	Q9PG72	Q9pg72 xylella fas
18	9	1.5	581	16	Q8Z3M5	Q8z3m5 salmonella
19	9	1.5	581	16	Q8FDG5	Q8fdg5 escherichia
20	9	1.5	582	16	Q8PFU7	Q8pfu7 xanthomonas
21	9	1.5	582	16	Q8P491	Q8p491 xanthomonas
22	9	1.5	582	16	Q8ZI70	Q8zi70 yersinia pe
23	9	1.5	589	16	Q8K812	Q8k812 streptococc
24	9	1.5	592	16	Q8DUS6	Q8dus6 streptococc
25	9	1.5	595	16	Q92FZ7	Q92fz7 rickettsia
26	9	1.5	595	16	Q8XIV5	Q8xiv5 clostridium
27	9	1.5	604	16	Q9A0G9	Q9a0g9 streptococc
28	9	1.5	604	16	Q8P1J0	Q8p1j0 streptococc
29	9	1.5	604	16	Q8EPY5	Q8epy5 oceanobacil
30	9	1.5	640	16	Q8YX92	Q8yx92 anabaena sp
31	9	1.5	760	5	Q9XZP7	Q9xzp7 caenorhabdi
32	8	1.3	81	2	Q47613	Q47613 escherichia
33	8	1.3	177	16	Q9CHP0	Q9chp0 lactococcus
34	8	1.3	295	16	Q97DH9	Q97dh9 clostridium
35	8	1.3	342	16	Q9CFI5	Q9cfi5 lactococcus
36	8	1.3	344	12	Q8V3G4	Q8v3g4 swinepox vi
37	8	1.3	350	16	Q9P9T7	Q9p9t7 xylella fas
38	8	1.3	351	17	Q8PTM2	Q8ptm2 methanosarc
39	8	1.3	432	10	Q9FZI8	Q9fzi8 arabidopsis
40	8	1.3	496	12	Q8B3S5	Q8b3s5 tick-borne
41	8	1.3	655	16	Q8FZK1	Q8fzk1 brucella su
42	8	1.3	680	5	O02325	O02325 caenorhabdi
43	8	1.3	681	16	Q8YIB4	Q8yib4 brucella me
44	8	1.3	867	13	Q90X49	Q90x49 brachydanio
45	8	1.3	958	13	Q8AXP2	Q8axp2 gallus gall

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 02:48:26 ; Search time 2774 Seconds  
(without alignments)  
5248.155 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 599  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141824\_27326/app\_query.fasta\_1.775  
-DB=EST -QFMT=fastap -SUFFIX=oli.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10025222@CGN\_1\_1\_3549@runat\_13112003\_141824\_27326 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*

```

18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query					Description	
No.	Score	Match	Length	DB	ID			
	1	10	1.7	545	28	BH246061	BH246061 pSB1678.1	
	2	10	1.7	899	29	BZ559622	BZ559622 pacs2-164	
c	3	10	1.7	1063	29	BZ549237	BZ549237 pacs1-60_	
	4	9	1.5	255	10	AW883813	AW883813 QV2-OT006	
c	5	9	1.5	299	10	BB179148	BB179148 BB179148	
c	6	9	1.5	308	10	BB188459	BB188459 BB188459	
c	7	9	1.5	350	9	AI663712	AI663712 ud47a09.y	
c	8	9	1.5	386	13	BY506458	BY506458 BY506458	
c	9	9	1.5	407	9	AI037711	AI037711 uh26c03.r	
c	10	9	1.5	474	12	BM871987	BM871987 mgmy001xG	
c	11	9	1.5	482	10	BF324020	BF324020 SnEST4a21	
	12	9	1.5	549	14	CA844844	CA844844 hab92e05.	
	13	9	1.5	567	10	BF707437	BF707437 EST1173 M	
c	14	9	1.5	580	28	AZ212308	AZ212308 Sheared D	
	15	9	1.5	602	13	BQ554692	BQ554692 H4029G06-	
	16	9	1.5	623	13	BU443069	BU443069 604146910	
c	17	9	1.5	631	28	AZ499451	AZ499451 1M0337009	
	18	9	1.5	639	12	BM194833	BM194833 L0701G07-	
	19	9	1.5	648	13	BU281567	BU281567 603865105	
	20	9	1.5	659	13	BU459287	BU459287 603775746	
	21	9	1.5	666	13	BU402231	BU402231 604137130	
c	22	9	1.5	689	29	BZ237979	BZ237979 CH230-373	
c	23	9	1.5	786	12	BI549191	BI549191 603189803	
	24	9	1.5	815	10	BF572162	BF572162 602076953	
c	25	9	1.5	828	29	CNS03E4U	AL239943 Tetraodon	
	26	9	1.5	852	29	CNS01P11	AL154229 Anopheles	
	27	9	1.5	910	14	CB181330	CB181330 AGENCOURT	
	28	9	1.5	993	29	BZ550385	BZ550385 pacs1-60_	
c	29	9	1.5	997	10	BF578695	BF578695 602093181	
	30	9	1.5	3268	28	BH770998	BH770998 LLMGtag72	
	31	8	1.3	130	9	AB029577	AB029577 AB029577	
	32	8	1.3	131	10	BF151025	BF151025 uy91d01.x	
c	33	8	1.3	134	9	AV081267	AV081267 AV081267	
	34	8	1.3	135	10	BF451163	BF451163 uz70g07.x	
	35	8	1.3	136	9	AV107325	AV107325 AV107325	
c	36	8	1.3	137	9	AA689916	AA689916 vt63b09.r	
c	37	8	1.3	138	9	AV131418	AV131418 AV131418	
	38	8	1.3	139	9	AW554854	AW554854 L0246D03-	
c	39	8	1.3	140	9	AA616261	AA616261 vo50f03.r	

c	40	8	1.3	140	13	BQ482116	BQ482116 ke49g01.y
c	41	8	1.3	141	9	AV164693	AV164693 AV164693
c	42	8	1.3	144	9	AV106216	AV106216 AV106216
	43	8	1.3	144	12	BM123705	BM123705 L0529B02-
c	44	8	1.3	146	9	AV106731	AV106731 AV106731
c	45	8	1.3	147	9	AV132246	AV132246 AV132246

5

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OM protein - protein search, using sw model

Run on: November 13, 2003, 23:16:13 ; Search time 69 Seconds  
(without alignments)  
1377.931 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 3109  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	3109	100.0	599	23	AAU98678	S. aureus STAAU_R9
2	2906	93.5	572	20	AAU49072	Amino acid sequenc
3	2906	93.5	572	22	AAB31938	Amino acid sequenc
4	2233.5	71.8	600	23	ABP38791	Staphylococcus epi
5	1054.5	33.9	626	23	ABB49107	Listeria monocytog
6	840.5	27.0	591	24	ABU01487	S. pneumoniae type
7	836	26.9	604	23	ABG61635	Streptococcus pyog
8	836	26.9	604	23	ABP27314	Streptococcus poly
9	833.5	26.8	591	20	AAU02246	A polypeptide of t
10	833.5	26.8	594	19	AAW80606	S. pneumoniae DNA
11	833	26.8	600	22	AAB31946	Amino acid sequenc
12	829	26.7	637	23	ABB53861	Lactococcus lactis
13	812	26.1	629	23	ABP27313	Streptococcus poly
14	650.5	20.9	590	24	ABU06094	N. meningitidis va
15	632.5	20.3	620	24	ABP79681	N. gonorrhoeae ami
16	627	20.2	646	22	AAU52123	Propionibacterium
17	564.5	18.2	529	18	AAW20994	H. pylori cytoplas
18	526	16.9	633	22	AAG92232	C glutamicum prote
19	518.5	16.7	590	22	AAM48181	Thermus thermophil
20	510.5	16.4	702	23	ABP65932	Bifidobacterium lo
21	358.5	11.5	428	23	ABU51831	Helicobacter pylor
22	348	11.2	403	23	ABU50968	Helicobacter pylor
23	302.5	9.7	402	20	AAU35597	Chlamydia pneumoni
24	286	9.2	203	20	AAU37348	Protein involved i
25	264.5	8.5	223	20	AAU37349	Protein involved i
26	239.5	7.7	214	23	ABU50770	Helicobacter pylor
27	239.5	7.7	216	21	AAB52593	Helicobacter pylor
28	234	7.5	207	20	AAU35596	Chlamydia pneumoni
29	195	6.3	39	23	AAU98680	S. aureus STAAU_R9
30	188	6.0	66	13	AAR23009	Macromolecular sys
31	164.5	5.3	92	13	AAR21562	Internal segment o
32	163	5.2	2295	21	AAB18180	Plasmodium falcipa
33	159	5.1	1010	23	ABP40333	Staphylococcus epi
34	156	5.0	1639	19	AAW54145	P. falciparum synt
35	156	5.0	1639	23	AAE29345	Plasmodium falcipa
36	153.5	4.9	1090	23	ABB54799	Lactococcus lactis
37	151	4.9	1979	21	AAB18171	Plasmodium falcipa
38	149.5	4.8	3210	24	ABU07438	Protein differenti
39	149.5	4.8	3248	17	AAR99795	Kinetochore protei
40	149	4.8	2017	22	ABG06301	Novel human diagno
41	148.5	4.8	69	23	ABP10181	Human ORFX protein
42	148	4.8	980	21	AAB18294	Plasmodium falcipa
43	148	4.8	1091	21	AAG38615	Arabidopsis thalia
44	148	4.8	1096	21	AAG38614	Arabidopsis thalia
45	148	4.8	1140	21	AAG38613	Arabidopsis thalia

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:18:03 ; Search time 41 Seconds  
(without alignments)  
618.151 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 3109  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2233.5	71.8	600	4	US-09-134-001C-3636	Sequence 3636, Ap
2	940.5	30.3	639	4	US-09-107-532A-4304	Sequence 4304, Ap
3	833.5	26.8	594	3	US-08-987-151-2	Sequence 2, Appli
4	731.5	23.5	698	4	US-09-252-991A-17456	Sequence 17456, A
5	610	19.6	622	4	US-09-328-352-4776	Sequence 4776, Ap
6	302.5	9.7	402	4	US-09-198-452A-1015	Sequence 1015, Ap
7	234	7.5	207	4	US-09-198-452A-1014	Sequence 1014, Ap
8	159	5.1	1010	4	US-09-134-001C-5178	Sequence 5178, Ap
9	149.5	4.8	3248	1	US-08-353-700-1	Sequence 1, Appli
10	149.5	4.8	3248	5	PCT-US95-16216-1	Sequence 1, Appli
11	146	4.7	2482	1	US-08-328-254-6	Sequence 6, Appli
12	144.5	4.6	1151	4	US-09-134-001C-3242	Sequence 3242, Ap
13	137	4.4	1031	4	US-09-914-259-24	Sequence 24, Appl
14	130	4.2	1147	3	US-08-470-260-5	Sequence 5, Appli
15	130	4.2	1147	3	US-08-471-491-5	Sequence 5, Appli
16	130	4.2	1147	3	US-08-466-662-5	Sequence 5, Appli



17	130	4.2	3289	2	US-08-477-451-2	Sequence 2, Appli
18	129.5	4.2	957	4	US-09-914-259-16	Sequence 16, Appl
19	129	4.1	990	2	US-08-392-625-20	Sequence 20, Appl
20	129	4.1	990	2	US-08-466-961A-20	Sequence 20, Appl
21	128	4.1	1786	3	US-08-973-462-8	Sequence 8, Appli
22	127.5	4.1	963	4	US-09-914-259-20	Sequence 20, Appl
23	127.5	4.1	2662	4	US-09-595-684B-31	Sequence 31, Appl
24	125.5	4.0	993	4	US-08-836-687B-30	Sequence 30, Appl
25	125.5	4.0	2366	1	US-08-480-604A-10	Sequence 10, Appl
26	125.5	4.0	2366	2	US-08-405-496A-10	Sequence 10, Appl
27	125.5	4.0	2366	3	US-08-915-136-10	Sequence 10, Appl
28	125.5	4.0	2366	4	US-08-957-310-10	Sequence 10, Appl
29	125.5	4.0	2366	4	US-10-011-366-10	Sequence 10, Appl
30	123.5	4.0	963	4	US-09-914-259-22	Sequence 22, Appl
31	123.5	4.0	2522	3	US-09-251-645-13	Sequence 13, Appl
32	122.5	3.9	3878	4	US-09-914-259-11	Sequence 11, Appl
33	122	3.9	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
34	121.5	3.9	456	4	US-09-134-001C-3772	Sequence 3772, Ap
35	121.5	3.9	800	2	US-08-488-940-4	Sequence 4, Appli
36	121.5	3.9	813	2	US-08-488-940-3	Sequence 3, Appli
37	121.5	3.9	1181	2	US-08-488-940-2	Sequence 2, Appli
38	121.5	3.9	1194	2	US-08-488-940-1	Sequence 1, Appli
39	120.5	3.9	1447	4	US-09-376-330-17	Sequence 17, Appl
40	120	3.9	342	4	US-09-107-532A-4845	Sequence 4845, Ap
41	120	3.9	1048	3	US-09-356-952-5	Sequence 5, Appli
42	120	3.9	1388	2	US-08-685-576-1	Sequence 1, Appli
43	119.5	3.8	930	4	US-09-134-001C-5314	Sequence 5314, Ap
44	119.5	3.8	956	4	US-09-134-001C-4452	Sequence 4452, Ap
45	119.5	3.8	1194	2	US-08-488-940-17	Sequence 17, Appl

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:18:54 ; Search time 67 Seconds  
(without alignments)  
1632.136 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 3109  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		Length	DB ID	Description
		Match	Length			
1	3109	100.0	599	15	US-10-025-222A-2	Sequence 2, Appli
2	2906	93.5	572	15	US-10-025-222A-39	Sequence 39, Appl
3	2906	93.5	572	16	US-10-282-287-12	Sequence 12, Appl
4	1018	32.7	603	15	US-10-025-222A-41	Sequence 41, Appl

5	886.5	28.5	597	15	US-10-025-222A-40	Sequence 40, Appl
6	626	20.1	581	15	US-10-025-222A-22	Sequence 22, Appl
7	604.5	19.4	632	15	US-10-156-761-13208	Sequence 13208, A
8	526	16.9	633	10	US-09-738-626-5986	Sequence 5986, Ap
9	302	9.7	98	15	US-10-025-222A-37	Sequence 37, Appl
10	195	6.3	39	15	US-10-025-222A-6	Sequence 6, Appli
11	156	5.0	1639	15	US-10-087-464-10	Sequence 10, Appl
12	143.5	4.6	1979	15	US-10-205-823-419	Sequence 419, App
13	137	4.4	1031	12	US-10-080-608A-24	Sequence 24, Appl
14	136.5	4.4	1184	9	US-09-815-242-5229	Sequence 5229, Ap
15	136.5	4.4	1188	9	US-09-815-242-12125	Sequence 12125, A
16	135.5	4.4	751	9	US-09-864-761-38419	Sequence 38419, A
17	130	4.2	773	9	US-09-815-242-11330	Sequence 11330, A
18	130	4.2	1338	9	US-09-402-100-4	Sequence 4, Appli
19	129.5	4.2	957	12	US-10-080-608A-16	Sequence 16, Appl
20	128	4.1	1786	10	US-09-742-096-3	Sequence 3, Appli
21	127.5	4.1	963	12	US-10-080-608A-20	Sequence 20, Appl
22	127	4.1	656	15	US-10-234-432-62	Sequence 62, Appl
23	127	4.1	1369	9	US-09-729-674-42	Sequence 42, Appl
24	126.5	4.1	930	9	US-09-815-242-10779	Sequence 10779, A
25	126.5	4.1	996	9	US-09-815-242-5251	Sequence 5251, Ap
26	126.5	4.1	1009	9	US-09-815-242-12141	Sequence 12141, A
27	126	4.1	1279	12	US-09-882-227-388	Sequence 388, App
28	126	4.1	1881	12	US-10-032-585-7646	Sequence 7646, Ap
29	125.5	4.0	337	12	US-10-097-111-295	Sequence 295, App
30	125.5	4.0	2366	15	US-10-011-366-10	Sequence 10, Appl
31	124.5	4.0	1805	11	US-09-820-843A-73	Sequence 73, Appl
32	123.5	4.0	963	12	US-10-080-608A-22	Sequence 22, Appl
33	123	4.0	2025	9	US-09-815-242-5703	Sequence 5703, Ap
34	123	4.0	3158	9	US-09-815-242-12611	Sequence 12611, A
35	122.5	3.9	700	10	US-09-881-752A-180	Sequence 180, App
36	122.5	3.9	1191	15	US-10-087-464-47	Sequence 47, Appl
37	122.5	3.9	2437	9	US-09-815-242-5834	Sequence 5834, Ap
38	122.5	3.9	3878	12	US-10-080-608A-11	Sequence 11, Appl
39	122.5	3.9	3899	15	US-10-171-311-4	Sequence 4, Appli
40	122.5	3.9	3907	15	US-10-171-311-2	Sequence 2, Appli
41	122.5	3.9	3917	15	US-10-171-311-8	Sequence 8, Appli
42	122.5	3.9	3925	15	US-10-171-311-6	Sequence 6, Appli
43	122.5	3.9	6281	9	US-09-815-242-12996	Sequence 12996, A
44	122	3.9	1038	12	US-10-032-585-7776	Sequence 7776, Ap
45	121.5	3.9	796	12	US-10-032-585-7201	Sequence 7201, Ap

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 00:25:50 ; Search time 5214 Seconds  
(without alignments)  
4699.821 Million cell updates/sec

Title: US-10-025-222A-2  
Perfect score: 3109  
Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYLYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141744\_26916/app\_query.fasta\_1.775  
-DB=GenEmbl -QFMT=fastap -SUFFIX=std.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10025222\_@CGN\_1\_1\_4958\_@runat\_13112003\_141744\_26916 -NCPUs=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*

```

18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	3109	100.0	1797	6	AX617520		AX617520	Sequence
	2	3109	100.0	1800	6	AX574337		AX574337	Sequence
c	3	3085	99.2	301550	1	AP003134		AP003134	Staphyloc
c	4	3085	99.2	346900	1	AP003362		AP003362	Staphyloc
c	5	3076	98.9	333750	1	AP004827		AP004827	Staphyloc
	6	3061	98.5	5910	1	AB001896		AB001896	Staphyloc
	7	2899	93.2	2687	6	AR149331		AR149331	Sequence
c	8	2233.5	71.8	300029	1	AE016748		AE016748	Staphyloc
c	9	1067.5	34.3	333050	1	AL596168		AL596168	Listeria
	10	1067.5	34.3	349980	6	AX413017		AX413017	Sequence
c	11	1067.5	34.3	349980	6	AX417044		AX417044	Sequence
	12	1056.5	34.0	3777	1	LMU13165		U13165	Listeria mo
c	13	1054.5	33.9	240050	1	AL591979		AL591979	Listeria
c	14	1054.5	33.9	349980	6	AX641668		AX641668	Sequence
c	15	1028	33.1	290029	1	AE017038		AE017038	Bacillus
	16	1025	33.0	2317	1	STAPLAC		M63177	S.aureus si
c	17	1021	32.8	301332	1	AE017012		AE017012	Bacillus
	18	1018	32.7	2001	1	BACDNAE		M10040	B.subtilis
	19	1018	32.7	5127	1	BSSIG43		X03897	Bacillus su
c	20	1018	32.7	213420	1	BSUB0014		Z99117	Bacillus su
c	21	1018	32.7	218470	1	BSUB0013		Z99116	Bacillus su
	22	1018	32.7	282700	1	BACJH642		D84432	Bacillus su
	23	988	31.8	2653	6	AX416557		AX416557	Sequence
	24	973.5	31.3	302173	1	AE016951		AE016951	Enterococ
	25	965.5	31.1	299550	1	AP001511		AP001511	Bacillus
c	26	908	29.2	302050	1	AL935257		AL935257	Lactobaci
c	27	897.5	28.9	300050	1	AP004599		AP004599	Oceanobac

	28	886.5	28.5	1794	1	AF106033	AF106033	Bacillus
	29	843	27.1	11919	1	AE010014	AE010014	Streptoco
	30	842.5	27.1	4643	1	AE014923	AE014923	Streptoco
	31	840.5	27.0	1773	6	AX568917	AX568917	Sequence
c	32	840.5	27.0	5406	6	AR218934	AR218934	Sequence
c	33	840.5	27.0	5406	6	BD003846	BD003846	Polynucle
	34	840.5	27.0	11293	1	AE007409	AE007409	Streptoco
	35	840.5	27.0	349980	6	AX571762	AX571762	Sequence
	36	840.5	27.0	349980	6	AX571763	AX571763	Sequence
	37	836	26.9	11919	1	AE006529	AE006529	Streptoco
	38	833.5	26.8	1785	6	AR136860	AR136860	Sequence
	39	833.5	26.8	1785	6	AR136861	AR136861	Sequence
	40	833.5	26.8	2748	6	E36414	E36414	dna G. 6/20
	41	833.5	26.8	10029	1	AE008471	AE008471	Streptoco
	42	831	26.7	51719	1	AE014147	AE014147	Streptoco
c	43	831	26.7	325650	1	AP005145	AP005145	Streptoco
	44	830.5	26.7	1701	6	AX433127	AX433127	Sequence
	45	829	26.7	12342	1	AE006289	AE006289	Lactococc

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 00:25:00 ; Search time 400 Seconds  
 (without alignments)  
 4042.408 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141743\_26906/app\_query.fasta\_1.775  
 -DB=N\_Geneseq\_19Jun03 -QFMT=fastap -SUFFIX=std.rng -MINMATCH=0.1 -LOOPCL=0  
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
 -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10025222 @CGN\_1\_1\_490 @runat\_13112003\_141743\_26906 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_19Jun03:\*  
 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*  
 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*  
 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*  
 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*  
 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*  
 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*  
 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*  
 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*  
 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*  
 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*  
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 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*  
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*  
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*  
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*  
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*  
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*  
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*  
 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	3109	100.0	1800	24	ABK87088	DNA encoding S. au
	2	2906	93.5	1719	20	AAZ31006	Partial dnaG gene.
	3	2906	93.5	1719	22	AAF54738	Nucleotide sequenc
	4	2899	93.2	2687	21	AAA26883	Essential Staphylo
	5	2899	93.2	2687	22	AAS08034	Staphylococcus aur
	6	2899	93.2	2687	22	AAF91565	Staphylococcus aur
	7	2233.5	71.8	1803	24	ABN91336	Staphylococcus epi
	8	1286	41.4	752	18	AAV75013	Staphylococcus aur
	9	1179	37.9	782	18	AAV75008	Staphylococcus aur
	10	1067.5	34.3	495269	24	ABQ67195	Listeria innocua c
c	11	1067.5	34.3	3011208	24	ABQ69245	Listeria innocua D
c	12	1054.5	33.9	2944528	24	ABA03041	Listeria monocytog
	13	988	31.8	2653	24	ABQ70735	Listeria monocytog
	14	973.5	31.3	7947	20	AAX13021	Enterococcus faeca
	15	973.5	31.3	7947	24	ABS98816	Enterococcus faeca
	16	840.5	27.0	1773	25	ABX06775	S. pneumoniae type
c	17	840.5	27.0	5406	19	AAV52299	Streptococcus pneu
	18	840.5	27.0	2162598	25	ABS56454	Streptococcus pneu
	19	836	26.9	1812	24	ABN67945	Streptococcus poly
	20	836	26.9	1815	22	AAF54746	Nucleotide sequenc
	21	833.5	26.8	1785	19	AAV65288	DNA encoding a S.
	22	833.5	26.8	2748	20	AAX35506	DNA encoding a pol
	23	830.5	26.7	1701	24	ABK74251	Bacillus lichenifo
	24	829	26.7	2365589	24	ABA90521	Genomic sequence o
	25	812	26.1	1887	24	ABN67944	Streptococcus poly
c	26	812	26.1	2155561	24	ABN71527	Streptococcus poly
	27	768	24.7	1206	24	ABK78652	Bacillus clausii g
	28	748.5	24.1	1602	19	AAV65278	DNA sequence of S.
	29	651.5	21.0	14652	21	AAA81482	N. meningitidis pa
	30	651.5	21.0	349980	21	AAF21611	Neisseria meningit
	31	651.5	21.0	837096	21	AAA81489	N. meningitidis pa
	32	650.5	20.9	1813	25	ABX09929	N. meningitidis DN
	33	640	20.6	1830121	17	AAT42063	Haemophilus influe
	34	632.5	20.3	1860	25	ABZ40651	N. gonorrhoeae nuc
c	35	627	20.2	37716	23	AAS59553	Propionibacterium
c	36	591.5	19.0	910715	20	AAX20248	Borrelia burgdorfe
	37	564.5	18.2	1587	18	AAT68247	H. pylori cytoplas
c	38	546	17.6	640681	24	ABA92787	Buchnera sp. genom
c	39	541.5	17.4	65792	22	AAF28544	Genomic fragment #
c	40	531.5	17.1	4403765	22	AAI99683	Mycobacterium tube
c	41	531.5	17.1	4411529	22	AAI99682	Mycobacterium tube
	42	526	16.9	1899	22	AAH67451	C glutamicum codin
	43	526	16.9	1899	25	ACA01249	C. glutamicum deri



c	44	526	16.9	349980	22	AAH68531	C glutamicum codin
c	45	525.5	16.9	1038602	20	AAZ01425	Complete genome se

GenCore version 5.1.6

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 00:27:00 ; Search time 107 Seconds  
 (without alignments)  
 2470.921 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYLYQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141745\_26947/app\_query.fasta\_1.775  
 -DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=std.rni -MINMATCH=0.1 -LOOPCL=0  
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
 -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10025222@cgn\_1\_1\_103@runat\_13112003\_141745\_26947 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2899	93.2	2687	3	US-08-714-918-34	Sequence 34, Appl

	2	2899	93.2	2687	3	US-09-265-315-34	Sequence 34, Appl
	3	2899	93.2	2687	3	US-09-265-315-34	Sequence 34, Appl
	4	2899	93.2	2687	3	US-09-266-417-34	Sequence 34, Appl
	5	2233.5	71.8	1803	4	US-09-134-001C-799	Sequence 799, App
	6	940.5	30.3	1920	4	US-09-107-532A-650	Sequence 650, App
c	7	840.5	27.0	5406	4	US-08-961-527-166	Sequence 166, App
	8	833.5	26.8	1785	3	US-08-987-151-1	Sequence 1, Appli
	9	833.5	26.8	1785	3	US-08-987-151-3	Sequence 3, Appli
	10	748.5	24.1	1602	3	US-08-987-151-4	Sequence 4, Appli
	11	731.5	23.5	2097	4	US-09-252-991A-885	Sequence 885, App
c	12	725	23.3	5659	4	US-09-221-017B-440	Sequence 440, App
	13	712.5	22.9	1788	4	US-09-252-991A-863	Sequence 863, App
	14	640	20.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
	15	640	20.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	16	610	19.6	1869	4	US-09-328-352-650	Sequence 650, App
c	17	531.5	17.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	18	531.5	17.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	19	506.5	16.3	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c	20	494.5	15.9	1533	4	US-09-252-991A-800	Sequence 800, App
c	21	337	10.8	580073	4	US-08-545-528D-1	Sequence 1, Appli
c	22	194.5	6.3	49272	1	US-08-614-770A-1	Sequence 1, Appli
c	23	184	5.9	50341	1	US-08-247-901C-1	Sequence 1, Appli
c	24	184	5.9	50341	2	US-09-075-904-1	Sequence 1, Appli
c	25	184	5.9	52297	3	US-09-426-436-1	Sequence 1, Appli
c	26	184	5.9	52297	4	US-08-705-557-1	Sequence 1, Appli
	27	166.5	5.4	8140	1	US-08-297-294A-1	Sequence 1, Appli
	28	159	5.1	3033	4	US-09-134-001C-2341	Sequence 2341, Ap
	29	149.5	4.8	5181	1	US-08-257-073-10	Sequence 10, Appl
	30	149.5	4.8	8789	1	US-08-328-254-5	Sequence 5, Appli
	31	149.5	4.8	10136	1	US-08-353-700-2	Sequence 2, Appli
	32	149.5	4.8	10136	5	PCT-US95-16216-2	Sequence 2, Appli
	33	144.5	4.6	3456	4	US-09-134-001C-405	Sequence 405, App
c	34	140	4.5	129908	4	US-09-585-858-1	Sequence 1, Appli
c	35	139.5	4.5	1028	4	US-08-858-207A-222	Sequence 222, App
	36	137	4.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	37	133	4.3	2478	4	US-09-601-198-52	Sequence 52, Appl
	38	132	4.2	4344	4	US-09-601-198-165	Sequence 165, App
	39	130.5	4.2	2389	1	US-08-480-552-18	Sequence 18, Appl
	40	130.5	4.2	2389	2	US-08-486-382-4	Sequence 4, Appli
	41	130.5	4.2	2389	3	US-09-235-546-4	Sequence 4, Appli
	42	130.5	4.2	2389	3	US-08-929-208-18	Sequence 18, Appl
	43	130.5	4.2	2389	4	US-09-568-315-18	Sequence 18, Appl
	44	130.5	4.2	2389	4	US-09-535-789-4	Sequence 4, Appli
	45	130	4.2	3763	1	US-07-792-865D-1	Sequence 1, Appli

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 00:27:45 ; Search time 500 Seconds  
 (without alignments)  
 3915.309 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKM 599

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141745\_26978/app\_query.fasta\_1.775  
 -DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1  
 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
 -MAXLEN=2000000000 -USER=US10025222\_@CGN\_1\_1\_107\_@runat\_13112003\_141745\_26978  
 -NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	3109	100.0	1800	14	US-10-025-222A-1	Sequence 1, Appli
2	2906	93.5	1719	15	US-10-282-287-11	Sequence 11, Appl
3	1319	42.4	782	8	US-08-781-986A-697	Sequence 697, App
4	1286	41.4	752	8	US-08-781-986A-702	Sequence 702, App
5	973.5	31.3	7947	10	US-09-070-927A-84	Sequence 84, Appl
6	830.5	26.7	1701	10	US-09-974-300-1542	Sequence 1542, Ap
7	768	24.7	1206	10	US-09-974-300-5943	Sequence 5943, Ap
8	640	20.6	1830121	14	US-10-329-960-1	Sequence 1, Appli
9	604.5	19.4	1896	14	US-10-156-761-5658	Sequence 5658, Ap
10	604.5	19.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 11	546	17.6	640681	10	US-09-790-988-1	Sequence 1, Appli
12	526	16.9	1899	10	US-09-738-626-2486	Sequence 2486, Ap
c 13	526	16.9	3309400	10	US-09-738-626-1	Sequence 1, Appli
14	337	10.8	38596	12	US-09-960-858-1	Sequence 1, Appli
15	337	10.8	38596	12	US-09-960-870-1	Sequence 1, Appli
c 16	337	10.8	580073	12	US-10-205-220-1	Sequence 1, Appli
17	199.5	6.4	403	10	US-09-764-877-486	Sequence 486, App
18	195	6.3	120	14	US-10-025-222A-5	Sequence 5, Appli
19	156	5.0	5917	14	US-10-087-464-9	Sequence 9, Appli
20	149.5	4.8	10096	10	US-09-960-253-163	Sequence 163, App
21	149	4.8	10190	10	US-09-864-864-292	Sequence 292, App
22	149	4.8	10211	10	US-09-954-456-1153	Sequence 1153, Ap
23	149	4.8	10211	10	US-09-967-768A-186	Sequence 186, App
24	149	4.8	10211	11	US-09-918-624B-2	Sequence 2, Appli
25	149	4.8	10281	12	US-10-240-965-201	Sequence 201, App
26	149	4.8	10281	14	US-10-084-817-361	Sequence 361, App
27	148.5	4.8	56506	12	US-10-097-111-10	Sequence 10, Appl
28	143.5	4.6	6452	14	US-10-205-823-418	Sequence 418, App
29	140.5	4.5	4780	9	US-09-962-436-287	Sequence 287, App
c 30	140	4.5	129908	14	US-10-270-875-1	Sequence 1, Appli
c 31	140	4.5	129908	14	US-10-270-878-1	Sequence 1, Appli
c 32	140	4.5	129908	14	US-10-270-786-1	Sequence 1, Appli
c 33	140	4.5	129908	14	US-10-270-710-1	Sequence 1, Appli
c 34	140	4.5	129908	14	US-10-270-859-1	Sequence 1, Appli
c 35	140	4.5	129908	15	US-10-270-846-1	Sequence 1, Appli
36	136.5	4.4	3552	9	US-09-815-242-4174	Sequence 4174, Ap
37	136.5	4.4	3567	9	US-09-815-242-8027	Sequence 8027, Ap
38	135.5	4.4	5967	14	US-10-171-581-158	Sequence 158, App
39	133.5	4.3	3825	10	US-09-974-300-219	Sequence 219, App
c 40	133.5	4.3	5247	10	US-09-070-927A-365	Sequence 365, App
c 41	133	4.3	2478	12	US-10-349-680-145	Sequence 145, App
42	132.5	4.3	6316	14	US-10-198-846-11287	Sequence 11287, A
43	132	4.2	4344	12	US-10-349-680-84	Sequence 84, Appl
44	131.5	4.2	7694	12	US-10-096-534-34	Sequence 34, Appl
45	131.5	4.2	8063	12	US-09-814-353-21776	Sequence 21776, A

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:16:59 ; Search time 43 Seconds  
 (without alignments)  
 1339.652 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_76:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3083	99.2	605	2	A89937	DNA primase [impor
2	1067.5	34.3	626	2	AC1619	DNA primase [impor
3	1054.5	33.9	626	2	AG1256	DNA primase [impor
4	1018	32.7	603	2	A22282	DNA primase (EC 2.
5	960.5	30.9	599	2	G83821	DNA primase dnaG [
6	840.5	27.0	586	2	H95123	DNA primase [impor
7	835	26.9	642	2	JC2485	DNA primase (EC 2.
8	833.5	26.8	591	2	B97994	DNA primase (EC 2.
9	829	26.7	637	2	H86693	DNA primase (EC 2.
10	801	25.8	596	2	I40609	DNA primase (EC 2.
11	801	25.8	596	2	C97060	DNA primase, DNAG
12	737	23.7	664	2	E83572	DNA primase PA0577
13	708.5	22.8	640	2	AH1971	DNA primase [impor
14	700.5	22.5	635	2	S75668	DNA primase (EC 2.
15	673.5	21.7	616	2	T11850	DNA primase (EC 2.
16	650.5	20.9	590	2	E81072	DNA primase NMB153
17	645	20.7	595	2	B97866	DNA primase (EC 2.
18	639	20.6	581	1	RYEBT	DNA primase (EC 2.

19	639	20.6	581	2	AI0892	DNA primase [impor
20	639	20.6	593	2	A64075	DNA primase (EC 2.
21	638	20.5	616	2	C71648	DNA primase (EC 2.
22	633.5	20.4	590	2	H81797	DNA primase (EC 2.
23	631	20.3	565	2	H72253	DNA primase - Ther
24	626	20.1	581	1	RYEC2	DNA primase (EC 2.
25	626	20.1	581	2	D85967	DNA biosynthesis,
26	626	20.1	581	2	E91122	DNA primase [impor
27	621	20.0	582	2	AG0079	DNA primase (EC 2.
28	607.5	19.5	571	2	A75499	DNA primase - Dein
29	595	19.1	498	2	G70429	DNA primase - Aqu
30	586.5	18.9	523	2	E70188	DNA primase (dnaG)
31	576	18.5	577	2	G82806	DNA primase XF0430
32	570.5	18.3	605	2	D71318	probable DNA prima
33	564.5	18.2	559	2	H71983	DNA primase - Heli
34	561.5	18.1	559	2	D64521	DNA primase - Heli
35	560.5	18.0	600	2	H81733	DNA primase TC0175
36	559	18.0	681	2	AD3318	DNA primase (EC 2.
37	554	17.8	595	2	F71471	probable DNA prima
38	546	17.6	577	2	C84936	DNA primase [impor
39	540.5	17.4	602	2	E90568	DNA primase [impor
40	535.5	17.2	605	2	D81260	DNA primase (EC 2.
41	531.5	17.1	639	2	H70661	probable dnaG prot
42	530.5	17.1	590	2	E72015	DNA primase - Chla
43	530.5	17.1	590	2	D86608	DNA primase [impor
44	530.5	17.1	594	2	A81525	DNA primase, proba
45	528.5	17.0	643	2	G87626	DNA primase [impor

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OM protein - protein search, using sw model

Run on: November 13, 2003, 23:38:38 ; Search time 38 Seconds  
 (without alignments)  
 741.289 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2906	93.5	572	1	PRIM_STAAU	O05338 staphylococ
2	1067.5	34.3	626	1	PRIM_LISIN	Q92bq5 listeria in
3	1054.5	33.9	626	1	PRIM_LISMO	P47762 listeria mo
4	1018	32.7	603	1	PRIM_BACSU	P05096 bacillus su
5	973.5	31.3	628	1	PRIM_ENTFA	P52308 enterococcu
6	960.5	30.9	599	1	PRIM_BACHD	Q9kd44 bacillus ha
7	886.5	28.5	597	1	PRIM_BACST	Q9x4d0 bacillus st
8	829	26.7	637	1	PRIM_LACLA	Q04505 lactococcus
9	801	25.8	596	1	PRIM_CLOAB	P33655 clostridium
10	738.5	23.8	660	1	PRIM_PSEPK	O33470 pseudomonas
11	737	23.7	664	1	PRIM_PSEAE	Q9i5w0 pseudomonas
12	700.5	22.5	635	1	PRIM_SYNY3	P74143 synechocyst
13	673.5	21.7	616	1	PRIM_SYNP7	P74893 synechococc
14	650.5	20.9	590	1	PRIM_NEIMB	P57029 neisseria m
15	639	20.6	581	1	PRIM_SALTY	P07362 salmonella
16	639	20.6	593	1	PRIM_HAEIN	Q08346 haemophilus
17	638	20.5	593	1	PRIM_RICPR	P30103 rickettsia
18	633.5	20.4	590	1	PRIM_NEIMA	P57028 neisseria m
19	631	20.3	565	1	PRIM_THEMA	Q9xlg3 thermotoga
20	626	20.1	581	1	PRIM_ECOLI	P02923 escherichia
21	620	19.9	576	1	PRIM_LEGPN	P71481 legionella
22	615.5	19.8	582	1	PRIM_PASMU	Q9cli9 pasteurella



23	607.5	19.5	571	1	PRIM_DEIRA	Q9rwr5	deinococcus
24	595	19.1	498	1	PRIM_AQUAE	O67465	aquifex aeo
25	588	18.9	578	1	PRIM_BUCBP	Q89b09	buchnera ap
26	586.5	18.9	523	1	PRIM_BORBU	O51653	borrelia bu
27	585	18.8	641	1	PRIM_STRCO	Q9sln4	streptomyce
28	570.5	18.3	605	1	PRIM_TREPA	O83505	treponema p
29	564.5	18.2	559	1	PRIM_HELPJ	Q9zn49	helicobacte
30	561.5	18.1	559	1	PRIM_HELPY	P56064	helicobacte
31	560.5	18.0	600	1	PRIM_CHLMU	Q9plc9	chlamydia m
32	555	17.9	636	1	PRIM_MYCSM	O52200	mycobacteri
33	554	17.8	595	1	PRIM_CHLTR	O84799	chlamydia t
34	546	17.6	577	1	PRIM_BUCAI	P57164	buchnera ap
35	540.5	17.4	602	1	PRIM_MYCPU	Q98qb3	mycoplasma
36	536	17.2	579	1	PRIM_BUCAP	P32000	buchnera ap
37	535.5	17.2	605	1	PRIM_CAMJE	Q9pm37	campylobact
38	531.5	17.1	639	1	PRIM_MYCTU	P95239	mycobacteri
39	530.5	17.1	590	1	PRIM_CHLPN	Q9z6w4	chlamydia p
40	525.5	16.9	606	1	PRIM_MYXXA	P50070	myxococcus
41	522.5	16.8	642	1	PRIM_MYCLE	Q9ccg2	mycobacteri
42	507	16.3	641	1	PRIM_UREPA	Q9ppz6	ureaplasma
43	436	14.0	620	1	PRIM_MYCPN	P75426	mycoplasma
44	345	11.1	607	1	PRIM_MYCGE	P47492	mycoplasma
45	156	5.0	1630	1	MSP1_PLAFK	P04932	plasmodium

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:10:54 ; Search time 71 Seconds  
 (without alignments)  
 2177.092 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL\_23:\*  
 1: sp\_archaea:\*  
 2: sp\_bacteria:\*  
 3: sp\_fungi:\*  
 4: sp\_human:\*  
 5: sp\_invertebrate:\*  
 6: sp\_mammal:\*  
 7: sp\_mhc:\*  
 8: sp\_organelle:\*  
 9: sp\_phage:\*  
 10: sp\_plant:\*  
 11: sp\_rodent:\*  
 12: sp\_virus:\*  
 13: sp\_vertebrate:\*  
 14: sp\_unclassified:\*  
 15: sp\_rvirus:\*  
 16: sp\_bacteriap:\*  
 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3083	99.2	605	16 Q99TT4	Q99tt4 staphylococ
2	3074	98.9	605	16 Q8NWB7	Q8nwb7 staphylococ
3	2231.5	71.8	598	16 Q8CP23	Q8cp23 staphylococ
4	897.5	28.9	604	16 Q8EPY5	Q8epy5 oceanobacil
5	843	27.1	604	16 Q8P1J0	Q8plj0 streptococc

6	841.5	27.1	592	16	Q8DUS6	Q8dus6 streptococc
7	840.5	27.0	586	16	Q97QX2	Q97qx2 streptococc
8	836	26.9	604	16	Q9A0G9	Q9a0g9 streptococc
9	833.5	26.8	591	16	Q8DPW1	Q8dpw1 streptococc
10	817	26.3	589	16	Q8K812	Q8k812 streptococc
11	812	26.1	602	16	Q8E4A4	Q8e4a4 streptococc
12	812	26.1	602	16	Q8DYP7	Q8dyp7 streptococc
13	792	25.5	595	16	Q8XIV5	Q8xiv5 clostridium
14	738	23.7	600	16	Q8R969	Q8r969 thermoanaer
15	734	23.6	643	2	Q8GDP9	Q8gdp9 heliobacill
16	731.5	23.5	603	16	Q8R623	Q8r623 fusobacteri
17	716	23.0	625	16	Q8KC38	Q8kc38 chlorobium
18	708.5	22.8	640	16	Q8YX92	Q8yx92 anabaena sp
19	653.5	21.0	574	16	Q8EHD9	Q8ehd9 shewanella
20	648	20.8	694	16	Q8DJB0	Q8djb0 synechococc
21	646	20.8	587	16	Q8DEG2	Q8deg2 vibrio vuln
22	645	20.7	595	16	Q92FZ7	Q92fz7 rickettsia
23	639	20.6	581	16	Q8Z3M5	Q8z3m5 salmonella
24	626	20.1	581	16	Q8FDG5	Q8fdg5 escherichia
25	623.5	20.1	598	16	Q8F416	Q8f416 leptospira
26	621	20.0	582	16	Q8ZI70	Q8zi70 yersinia pe
27	620	19.9	603	16	Q8XXA0	Q8xxa0 ralstonia s
28	583.5	18.8	628	2	Q9EZB7	Q9ezb7 zymomonas m
29	579	18.6	582	16	Q8P491	Q8p491 xanthomonas
30	576	18.5	577	16	Q9PG72	Q9pg72 xylella fas
31	575.5	18.5	667	16	Q92N97	Q92n97 rhizobium m
32	572	18.4	582	16	Q8PFU7	Q8pfu7 xanthomonas
33	565	18.2	688	16	Q8EW63	Q8ew63 mycoplasma
34	563	18.1	655	16	Q8FZK1	Q8fzk1 brucella su
35	559.5	18.0	652	16	Q98IC4	Q98ic4 rhizobium l
36	559	18.0	681	16	Q8YIB4	Q8yib4 brucella me
37	532	17.1	582	16	Q8D285	Q8d285 wiggleswort
38	528.5	17.0	643	16	Q9A401	Q9a401 caulobacter
39	526	16.9	633	16	Q8NND6	Q8nnd6 corynebacte
40	525.5	16.9	661	16	Q8UDF9	Q8udf9 agrobacteri
41	516.5	16.6	645	16	Q8FNH5	Q8fnh5 corynebacte
42	510.5	16.4	702	16	Q8G573	Q8g573 bifidobacte
43	324	10.4	925	2	Q8GDM3	Q8gdm3 photorhabdu
44	318	10.2	651	10	Q9AW16	Q9aw16 guillardia
45	211	6.8	81	2	Q47613	Q47613 escherichia

GenCore version 5.1.6

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 00:26:25 ; Search time 2775 Seconds  
 (without alignments)  
 5246.263 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 3109  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141744\_26928/app\_query.fasta\_1.775  
 -DB=EST -QFMT=fastap -SUFFIX=std.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10025222\_@CGN\_1\_1\_3549\_@runat\_13112003\_141744\_26928 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
 1: em\_estba:\*  
 2: em\_esthum:\*  
 3: em\_estin:\*  
 4: em\_estmu:\*  
 5: em\_estov:\*  
 6: em\_estpl:\*  
 7: em\_estro:\*  
 8: em\_htc:\*  
 9: gb\_est1:\*  
 10: gb\_est2:\*  
 11: gb\_htc:\*  
 12: gb\_est3:\*  
 13: gb\_est4:\*  
 14: gb\_est5:\*  
 15: em\_estfun:\*  
 16: em\_estom:\*  
 17: em\_gss\_hum:\*

```

18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length					
c	1	720	23.2	3268	28	BH770998	BH770998	LLMGtag72
	2	436.5	14.0	1063	29	BZ549237	BZ549237	pacs1-60_
	3	435.5	14.0	852	29	CNS01P11	AL154229	Anopheles
	4	361.5	11.6	545	28	BH246061	BH246061	pSB1678.1
	5	345.5	11.1	707	29	CNS01QS6	AL156502	Anopheles
	6	340	10.9	1405	29	BZ557385	BZ557385	pacs1-60_
	7	308.5	9.9	899	29	BZ559622	BZ559622	pacs2-164
	8	299	9.6	689	28	BH825304	BH825304	BACPP21-F
c	9	281.5	9.1	624	29	BZ551465	BZ551465	pacs1-60_
c	10	261	8.4	698	28	AQ989861	AQ989861	Rfc00521
	11	260	8.4	607	28	BH834041	BH834041	BACPP6-C1
	12	254.5	8.2	577	28	BH830643	BH830643	BACPP31-H
c	13	254	8.2	565	28	BH235113	BH235113	MSAD_B12.
	14	244	7.8	993	29	BZ550385	BZ550385	pacs1-60_
	15	240	7.7	468	29	CNS07F1E	AL607892	Anopheles
	16	179	5.8	572	28	AQ991213	AQ991213	Rfc02100
	17	158	5.1	586	28	BH861075	BH861075	S10D7T7 W
c	18	156.5	5.0	277	29	BZ295302	BZ295302	CG1410.r1
c	19	151	4.9	445	29	P212R	AL161311	Leishmani
c	20	148	4.8	1366	29	BZ564161	BZ564161	pacs2-164
	21	135.5	4.4	764	28	AQ990443	AQ990443	Rfc01215
	22	123	4.0	999	29	CNS06LJ5	AL404247	T3 end of
	23	121	3.9	2285	11	AK029513	AK029513	Mus muscu
	24	121	3.9	2740	11	AK029960	AK029960	Mus muscu
	25	119	3.8	3035	11	AK046231	AK046231	Mus muscu
	26	118.5	3.8	2815	11	BC024600	BC024600	Homo sapi
	27	117	3.8	4364	11	AK076392	AK076392	Mus muscu
	28	116	3.7	891	28	AZ535562	AZ535562	ENTBX24TR
	29	113.5	3.7	3336	11	AK029534	AK029534	Mus muscu
	30	113.5	3.7	3398	11	BC045617	BC045617	Mus muscu
	31	112.5	3.6	2062	11	AK005440	AK005440	Mus muscu
	32	112	3.6	2310	8	BC012585	BC012585	Homo sapi
	33	112	3.6	3093	11	AK045517	AK045517	Mus muscu
	34	112	3.6	3411	11	AK035509	AK035509	Mus muscu
	35	111.5	3.6	1100	29	CNS001EG	AL060701	Drosophil
c	36	111	3.6	785	28	AY080435	AY080435	AY080435
	37	111	3.6	2972	9	AW342118	AW342118	Sfc10 Mou
	38	110.5	3.6	3150	11	AK088733	AK088733	Mus muscu
	39	110.5	3.6	3953	11	AK052535	AK052535	Mus muscu

	40	110	3.5	2109	11	AK031918	AK031918 Mus muscu
	41	110	3.5	2800	11	BC021363	BC021363 Mus muscu
	42	110	3.5	2971	11	AK004574	AK004574 Mus muscu
c	43	109.5	3.5	930	29	CNS0709C	AL423334 T3 end of
	44	109.5	3.5	3511	11	BC030787	BC030787 Homo sapi
	45	109	3.5	468	10	BF052937	BF052937 EST438167

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:19:09 ; Search time 47 Seconds  
 (without alignments)  
 2022.920 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*  
 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*  
 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*  
 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*  
 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*  
 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*  
 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*  
 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*  
 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*  
 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*  
 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*  
 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*  
 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*  
 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*  
 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*  
 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*  
 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*  
 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*  
 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*  
 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*  
 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*  
 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*  
 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*  
 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*  
 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

No.	Score	Match Length	DB	ID	Description	
1	599	100.0	599	23	AAU98678	S. aureus STAAU_R9
2	290	48.4	572	20	AAU49072	Amino acid sequenc
3	290	48.4	572	22	AAB31938	Amino acid sequenc
4	64	10.7	600	23	ABP38791	Staphylococcus epi
5	39	6.5	39	23	AAU98680	S. aureus STAAU_R9
6	13	2.2	646	22	AAU52123	Propionibacterium
7	11	1.8	223	20	AAU37349	Protein involved i
8	10	1.7	10	23	AAU98681	Tryptic-digested p
9	10	1.7	626	23	ABB49107	Listeria monocytog
10	10	1.7	702	23	ABP65932	Bifidobacterium lo
11	9	1.5	66	13	AAR23009	Macromolecular sys
12	9	1.5	69	23	ABP10181	Human ORFX protein
13	9	1.5	73	22	ABB03562	Human musculoskele
14	9	1.5	73	24	ABU12856	Novel human muscul
15	9	1.5	106	21	AAG48564	Arabidopsis thalia
16	9	1.5	123	21	AAG48563	Arabidopsis thalia
17	9	1.5	183	21	AAG33065	Arabidopsis thalia
18	9	1.5	197	21	AAG33064	Arabidopsis thalia
19	9	1.5	214	21	AAG33063	Arabidopsis thalia
20	9	1.5	412	21	AAG48540	Arabidopsis thalia
21	9	1.5	414	21	AAG48539	Arabidopsis thalia
22	9	1.5	447	21	AAG48538	Arabidopsis thalia
23	9	1.5	452	23	AAU93194	Arabidopsis transc
24	9	1.5	458	21	AAG47240	Arabidopsis thalia
25	9	1.5	460	21	AAG47239	Arabidopsis thalia
26	9	1.5	493	21	AAG47238	Arabidopsis thalia
27	9	1.5	600	22	AAB31946	Amino acid sequenc
28	9	1.5	604	23	ABG61635	Streptococcus pyog
29	9	1.5	604	23	ABP27314	Streptococcus poly
30	9	1.5	637	23	ABB53861	Lactococcus lactis
31	9	1.5	760	23	AAU81524	C. elegans Che-2 p
32	8	1.3	176	23	ABB54001	Lactococcus lactis
33	8	1.3	342	23	ABB54834	Lactococcus lactis
34	8	1.3	387	21	AAB24263	Arabidopsis thalia
35	8	1.3	410	21	AAG22981	Arabidopsis thalia
36	8	1.3	410	21	AAG42648	Arabidopsis thalia
37	8	1.3	413	21	AAG22980	Arabidopsis thalia
38	8	1.3	413	21	AAG42647	Arabidopsis thalia
39	8	1.3	432	21	AAB24260	Arabidopsis thalia
40	8	1.3	432	21	AAB01212	Arabidopsis thalia
41	8	1.3	432	21	AAG22979	Arabidopsis thalia
42	8	1.3	432	21	AAG42646	Arabidopsis thalia
43	8	1.3	432	22	AAU00458	Arabidopsis thalia
44	8	1.3	1082	22	ABG12317	Novel human diagno
45	8	1.3	1159	22	AAU35496	Haemophilus influ



GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:23:29 ; Search time 21 Seconds  
 (without alignments)  
 1206.867 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYLLQQIVAKNKERM 599

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query						
No.	Score	Match	Length	DB	ID	Description	
1	64	10.7	600	4	US-09-134-001C-3636	Sequence 3636, Ap	
2	10	1.7	698	4	US-09-252-991A-17456	Sequence 17456, A	
3	9	1.5	639	4	US-09-107-532A-4304	Sequence 4304, Ap	
4	8	1.3	263	4	US-09-328-352-6598	Sequence 6598, Ap	
5	7	1.2	78	4	US-09-252-991A-18643	Sequence 18643, A	
6	7	1.2	84	4	US-09-328-352-7200	Sequence 7200, Ap	
7	7	1.2	107	4	US-09-134-001C-2988	Sequence 2988, Ap	
8	7	1.2	114	4	US-09-205-258-739	Sequence 739, App	
9	7	1.2	143	4	US-09-134-001C-3963	Sequence 3963, Ap	
10	7	1.2	218	4	US-09-328-352-4680	Sequence 4680, Ap	
11	7	1.2	235	4	US-09-205-258-318	Sequence 318, App	
12	7	1.2	235	4	US-09-205-258-738	Sequence 738, App	
13	7	1.2	238	4	US-09-328-352-5013	Sequence 5013, Ap	
14	7	1.2	241	4	US-09-328-352-8001	Sequence 8001, Ap	
15	7	1.2	249	4	US-09-134-001C-5578	Sequence 5578, Ap	
16	7	1.2	288	4	US-09-252-991A-29966	Sequence 29966, A	

17	7	1.2	309	3	US-08-969-644-20	Sequence 20, Appl
18	7	1.2	309	3	US-08-444-189-20	Sequence 20, Appl
19	7	1.2	309	3	US-08-468-544-20	Sequence 20, Appl
20	7	1.2	319	4	US-09-107-532A-5122	Sequence 5122, Ap
21	7	1.2	400	4	US-09-434-690-2	Sequence 2, Appli
22	7	1.2	400	4	US-09-511-964-2	Sequence 2, Appli
23	7	1.2	452	4	US-09-284-768A-22	Sequence 22, Appl
24	7	1.2	484	3	US-08-913-578-2	Sequence 2, Appli
25	7	1.2	484	3	US-08-785-427-2	Sequence 2, Appli
26	7	1.2	544	1	US-08-472-028A-8	Sequence 8, Appli
27	7	1.2	544	2	US-08-808-931-8	Sequence 8, Appli
28	7	1.2	544	3	US-08-808-323-8	Sequence 8, Appli
29	7	1.2	544	3	US-09-050-603A-8	Sequence 8, Appli
30	7	1.2	544	3	US-09-102-420B-8	Sequence 8, Appli
31	7	1.2	544	3	US-09-071-296-8	Sequence 8, Appli
32	7	1.2	544	3	US-09-196-268-8	Sequence 8, Appli
33	7	1.2	544	3	US-09-015-683-8	Sequence 8, Appli
34	7	1.2	544	4	US-09-191-998-8	Sequence 8, Appli
35	7	1.2	544	4	US-09-497-698-8	Sequence 8, Appli
36	7	1.2	552	3	US-09-120-365-5	Sequence 5, Appli
37	7	1.2	552	3	US-09-515-039-5	Sequence 5, Appli
38	7	1.2	567	2	US-08-504-459-2	Sequence 2, Appli
39	7	1.2	569	4	US-09-107-532A-6689	Sequence 6689, Ap
40	7	1.2	580	4	US-09-327-984A-38	Sequence 38, Appl
41	7	1.2	594	3	US-08-987-151-2	Sequence 2, Appli
42	7	1.2	608	4	US-09-284-768A-4	Sequence 4, Appli
43	7	1.2	613	4	US-09-252-991A-21411	Sequence 21411, A
44	7	1.2	657	4	US-09-284-768A-7	Sequence 7, Appli
45	7	1.2	729	4	US-09-252-991A-22350	Sequence 22350, A

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 14, 2003, 00:24:29 ; Search time 36 Seconds  
 (without alignments)  
 3037.587 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	599	100.0	599	15	US-10-025-222A-2	Sequence 2, Appli
2	290	48.4	572	15	US-10-025-222A-39	Sequence 39, Appl
3	290	48.4	572	16	US-10-282-287-12	Sequence 12, Appl
4	39	6.5	39	15	US-10-025-222A-6	Sequence 6, Appli

5	17	2.8	17	15	US-10-025-222A-36	Sequence 36, Appl
6	16	2.7	16	15	US-10-025-222A-35	Sequence 35, Appl
7	13	2.2	98	15	US-10-025-222A-37	Sequence 37, Appl
8	12	2.0	12	15	US-10-025-222A-34	Sequence 34, Appl
9	11	1.8	11	15	US-10-025-222A-32	Sequence 32, Appl
10	10	1.7	10	15	US-10-025-222A-30	Sequence 30, Appl
11	10	1.7	10	15	US-10-025-222A-31	Sequence 31, Appl
12	10	1.7	10	15	US-10-025-222A-33	Sequence 33, Appl
13	9	1.5	9	15	US-10-025-222A-29	Sequence 29, Appl
14	9	1.5	73	10	US-09-764-877-1509	Sequence 1509, Ap
15	9	1.5	452	11	US-09-934-455-516	Sequence 516, App
16	9	1.5	581	15	US-10-025-222A-22	Sequence 22, Appl
17	9	1.5	597	15	US-10-025-222A-40	Sequence 40, Appl
18	9	1.5	632	15	US-10-156-761-13208	Sequence 13208, A
19	9	1.5	760	10	US-09-866-582-42	Sequence 42, Appl
20	8	1.3	1159	9	US-09-815-242-11089	Sequence 11089, A
21	7	1.2	88	15	US-10-106-698-4886	Sequence 4886, Ap
22	7	1.2	101	11	US-09-764-891-3685	Sequence 3685, Ap
23	7	1.2	114	12	US-09-933-767-739	Sequence 739, App
24	7	1.2	114	15	US-10-023-282-739	Sequence 739, App
25	7	1.2	119	12	US-10-252-945-50	Sequence 50, Appl
26	7	1.2	143	11	US-09-764-891-4060	Sequence 4060, Ap
27	7	1.2	147	12	US-10-389-853-13	Sequence 13, Appl
28	7	1.2	202	12	US-10-389-853-12	Sequence 12, Appl
29	7	1.2	235	12	US-09-933-767-318	Sequence 318, App
30	7	1.2	235	12	US-09-933-767-738	Sequence 738, App
31	7	1.2	235	15	US-10-023-282-318	Sequence 318, App
32	7	1.2	235	15	US-10-023-282-738	Sequence 738, App
33	7	1.2	258	9	US-09-764-853-840	Sequence 840, App
34	7	1.2	258	15	US-10-091-438-205	Sequence 205, App
35	7	1.2	261	9	US-09-764-853-669	Sequence 669, App
36	7	1.2	261	15	US-10-091-438-144	Sequence 144, App
37	7	1.2	307	12	US-10-389-853-11	Sequence 11, Appl
38	7	1.2	341	11	US-09-948-820-48	Sequence 48, Appl
39	7	1.2	349	15	US-10-156-761-14185	Sequence 14185, A
40	7	1.2	361	15	US-10-149-819-10	Sequence 10, Appl
41	7	1.2	362	10	US-09-870-759-80	Sequence 80, Appl
42	7	1.2	362	12	US-09-751-708A-80	Sequence 80, Appl
43	7	1.2	400	15	US-10-126-170-2	Sequence 2, Appli
44	7	1.2	416	12	US-10-389-853-4	Sequence 4, Appli
45	7	1.2	431	12	US-10-311-626-9	Sequence 9, Appli

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 02:27:02 ; Search time 5213 Seconds  
 (without alignments)  
 4700.723 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
 Xgapop 60.0 , Xgapext 60.0  
 Ygapop 60.0 , Ygapext 60.0  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5773140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141823\_27313/app\_query.fasta\_1.775  
 -DB=GenEmbl -QFMT=fastap -SUFFIX=oli.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10025222@CGN\_1\_1\_4958@runat\_13112003\_141823\_27313 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_htg:\*  
 3: gb\_in:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pl:\*  
 9: gb\_pr:\*  
 10: gb\_ro:\*  
 11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*  
 15: em\_ba:\*  
 16: em\_fun:\*  
 17: em\_hum:\*

18: em\_in:\*  
 19: em\_mu:\*  
 20: em\_om:\*  
 21: em\_or:\*  
 22: em\_ov:\*  
 23: em\_pat:\*  
 24: em\_ph:\*  
 25: em\_pl:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	599	100.0	1797	6	AX617520	AX617520 Sequence
	2	599	100.0	1800	6	AX574337	AX574337 Sequence
c	3	324	54.1	301550	1	AP003134	AP003134 Staphyloc
c	4	324	54.1	346900	1	AP003362	AP003362 Staphyloc
	5	311	51.9	5910	1	AB001896	AB001896 Staphyloc
	6	207	34.6	2687	6	AR149331	AR149331 Sequence
c	7	201	33.6	333750	1	AP004827	AP004827 Staphyloc
	8	163	27.2	2317	1	STAPLAC	M63177 S.aureus si
c	9	64	10.7	300029	1	AE016748	AE016748 Staphyloc
	10	39	6.5	120	6	AX574341	AX574341 Sequence
	11	13	2.2	5168	1	AF027507	AF027507 Mycobacte
	12	13	2.2	300300	1	AP005373	AP005373 Thermosyn
	13	12	2.0	1206	6	AX437528	AX437528 Sequence
	14	12	2.0	1929	1	AY142927	AY142927 Helioinci
c	15	12	2.0	10625	1	AE015572	AE015572 Shewanell
c	16	12	2.0	11198	1	AE004138	AE004138 Vibrio ch
c	17	12	2.0	290029	1	AE017038	AE017038 Bacillus
c	18	12	2.0	298900	1	AP005074	AP005074 Vibrio pa
	19	12	2.0	301235	1	AE016799	AE016799 Vibrio vu
c	20	12	2.0	301332	1	AE017012	AE017012 Bacillus
c	21	12	2.0	333050	1	AL596168	AL596168 Listeria
	22	12	2.0	349980	6	AX413017	AX413017 Sequence
c	23	12	2.0	349980	6	AX417044	AX417044 Sequence
	24	11	1.8	10941	1	AE001351	AE001351 Chlamydia
	25	11	1.8	10949	1	AE002284	AE002284 Chlamydia
c	26	11	1.8	128598	1	D90912	D90912 Synechocyst
c	27	11	1.8	200050	1	AL646068	AL646068 Ralstonia

	28	11	1.8	299550	1	AP001511	AP001511 Bacillus
c	29	11	1.8	301439	1	AE015943	AE015943 Clostridi
	30	10	1.7	1701	6	AX433127	AX433127 Sequence
	31	10	1.7	1983	1	PPU85774	U85774 Pseudomonas
	32	10	1.7	2193	1	SYNDNAG	X94247 Synechococc
	33	10	1.7	2653	6	AX416557	AX416557 Sequence
	34	10	1.7	3777	1	LMU13165	U13165 Listeria mo
	35	10	1.7	4905	1	AF014397	AF014397 Pseudomon
c	36	10	1.7	10352	1	AE014738	AE014738 Bifidobac
c	37	10	1.7	12422	1	AE004494	AE004494 Pseudomon
c	38	10	1.7	15663	1	AE001796	AE001796 Thermotog
	39	10	1.7	18366	1	AF299295	AF299295 Zymomonas
c	40	10	1.7	240050	1	AL591979	AL591979 Listeria
c	41	10	1.7	300511	1	AE016775	AE016775 Pseudomon
c	42	10	1.7	302050	1	AL935257	AL935257 Lactobaci
	43	10	1.7	302050	1	BX321856	BX321856 Nitrosomo
c	44	10	1.7	334108	1	AE016857	AE016857 Pseudomon
c	45	10	1.7	349980	6	AX492785	AX492785 Sequence

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 01:25:41 ; Search time 398 Seconds  
 (without alignments)  
 4062.722 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
 Xgapop 60.0 , Xgapext 60.0  
 Ygapop 60.0 , Ygapext 60.0  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103488

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10025222/runat_13112003_141823_27303/app_query.fasta_1.775
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=oli.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10025222@CGN_1_1_490@runat_13112003_141823_27303 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Database : N\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*



18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*  
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*  
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*  
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*  
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*  
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*  
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*  
 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	599	100.0	1800	24	ABK87088		DNA encoding S. au
2	290	48.4	1719	20	AAZ31006		Partial dnaG gene.
3	290	48.4	1719	22	AAF54738		Nucleotide sequenc
4	210	35.1	752	18	AAV75013		Staphylococcus aur
5	207	34.6	2687	21	AAA26883		Essential Staphylo
6	207	34.6	2687	22	AAS08034		Staphylococcus aur
7	207	34.6	2687	22	AAF91565		Staphylococcus aur
8	149	24.9	782	18	AAV75008		Staphylococcus aur
9	64	10.7	1803	24	ABN91336		Staphylococcus epi
10	39	6.5	120	24	ABK87090		DNA encoding S. au
c 11	13	2.2	37716	23	AAS59553		Propionibacterium
12	12	2.0	1206	24	ABK78652		Bacillus clausii g
13	12	2.0	495269	24	ABQ67195		Listeria innocua c
c 14	12	2.0	3011208	24	ABQ69245		Listeria innocua D
c 15	11	1.8	1038602	20	AAZ01425		Complete genome se
16	10	1.7	1701	24	ABK74251		Bacillus lichenifo
17	10	1.7	2653	24	ABQ70735		Listeria monocytog
c 18	10	1.7	349980	24	ABQ81847		Bifidobacterium lo
c 19	10	1.7	2944528	24	ABA03041		Listeria monocytog
20	9	1.5	207	24	ABN25933		Human ORFX polynuc
21	9	1.5	403	22	AAL35144		Human musculoskele
22	9	1.5	403	25	ABX58132		cDNA encoding nove
23	9	1.5	548	13	AAQ21653		Macromolecular sys
c 24	9	1.5	648	22	AAH32164		Human olfactory re
c 25	9	1.5	933	22	AAH32118		Human olfactory re
c 26	9	1.5	936	22	AAS42443		Human cDNA encodin
c 27	9	1.5	936	24	ABZ43127		Human GPCR polynuc
c 28	9	1.5	936	24	ABK68450		Human DNA for olfa
c 29	9	1.5	936	24	ABK37729		DNA encoding G-cou
c 30	9	1.5	936	24	ABK16621		Human G-coupled re
c 31	9	1.5	936	25	ABZ77872		Human G protein co
c 32	9	1.5	940	24	ABK33474		Human cDNA encodin
33	9	1.5	1012	21	AAC49486		Arabidopsis thalia
c 34	9	1.5	1021	24	ABK33472		Human cDNA encodin
c 35	9	1.5	1021	24	ABK33473		Human cDNA encodin
36	9	1.5	1344	21	AAC49477		Arabidopsis thalia
37	9	1.5	1359	24	ABK65380		Arabidopsis cDNA e
38	9	1.5	1767	21	AAC48989		Arabidopsis thalia
39	9	1.5	1768	21	AAC43652		Arabidopsis thalia
40	9	1.5	1812	24	ABN67945		Streptococcus poly
41	9	1.5	1815	22	AAF54746		Nucleotide sequenc
42	9	1.5	7947	20	AAX13021		Enterococcus faeca
43	9	1.5	7947	24	ABS98816		Enterococcus faeca

c	44	9	1.5	640681	24	ABA92787	Buchnera sp. genom
	45	9	1.5	1830121	17	AAT42063	Haemophilus influe

GenCore version 5.1.6

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 14, 2003, 03:15:57 ; Search time 108 Seconds  
 (without alignments)  
 2448.042 Million cell updates/sec

Title: US-10-025-222A-2  
 Perfect score: 599  
 Sequence: 1 LRIDQSIINEIKDKTDILDL.....DVELQKYYLQQIVAKNKERM 599

Scoring table: OLIGO  
 Xgapop 60.0 , Xgapext 60.0  
 Ygapop 60.0 , Ygapext 60.0  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135288

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
 -Q=/cgn2\_1/USPTO\_spool\_p/US10025222/runat\_13112003\_141824\_27341/app\_query.fasta\_1.775  
 -DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=oli.rni -MINMATCH=0.1 -LOOPCL=0  
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi  
 -LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10025222\_@CGN\_1\_1\_103\_@runat\_13112003\_141824\_27341 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	207	34.6	2687	3	US-08-714-918-34	Sequence 34, Appl

	2	207	34.6	2687	3	US-09-265-315-34	Sequence 34, Appl
	3	207	34.6	2687	3	US-09-265-315-34	Sequence 34, Appl
	4	207	34.6	2687	3	US-09-266-417-34	Sequence 34, Appl
	5	64	10.7	1803	4	US-09-134-001C-799	Sequence 799, App
c	6	10	1.7	1533	4	US-09-252-991A-800	Sequence 800, App
	7	10	1.7	1788	4	US-09-252-991A-863	Sequence 863, App
	8	10	1.7	2097	4	US-09-252-991A-885	Sequence 885, App
	9	9	1.5	1920	4	US-09-107-532A-650	Sequence 650, App
	10	9	1.5	1830121	4	US-09-557-884-1	Sequence 1, Appli
	11	9	1.5	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	12	8	1.3	792	4	US-09-328-352-2472	Sequence 2472, Ap
	13	8	1.3	819	4	US-10-083-304-3	Sequence 3, Appli
c	14	8	1.3	1396	4	US-08-936-165A-242	Sequence 242, App
c	15	8	1.3	2722	4	US-09-390-234-13	Sequence 13, Appl
c	16	8	1.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	17	8	1.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	18	7	1.2	86	2	US-08-477-527A-138	Sequence 138, App
	19	7	1.2	86	3	US-08-481-710-138	Sequence 138, App
	20	7	1.2	86	5	PCT-US96-09537-138	Sequence 138, App
	21	7	1.2	237	4	US-09-252-991A-2072	Sequence 2072, Ap
	22	7	1.2	255	4	US-09-328-352-3074	Sequence 3074, Ap
	23	7	1.2	324	4	US-09-134-001C-151	Sequence 151, App
c	24	7	1.2	371	5	PCT-US93-08386-6	Sequence 6, Appli
c	25	7	1.2	419	4	US-09-702-705-1299	Sequence 1299, Ap
	26	7	1.2	419	4	US-09-702-705-1772	Sequence 1772, Ap
c	27	7	1.2	419	4	US-09-736-457-1299	Sequence 1299, Ap
	28	7	1.2	419	4	US-09-736-457-1772	Sequence 1772, Ap
	29	7	1.2	432	4	US-09-134-001C-1126	Sequence 1126, Ap
c	30	7	1.2	441	4	US-09-328-352-3809	Sequence 3809, Ap
	31	7	1.2	447	4	US-09-252-991A-5816	Sequence 5816, Ap
c	32	7	1.2	453	4	US-09-486-580A-2	Sequence 2, Appli
c	33	7	1.2	476	4	US-09-651-169A-38	Sequence 38, Appl
	34	7	1.2	495	4	US-09-506-729-46	Sequence 46, Appl
c	35	7	1.2	647	4	US-09-495-050A-54	Sequence 54, Appl
	36	7	1.2	657	4	US-09-328-352-554	Sequence 554, App
c	37	7	1.2	678	4	US-09-328-352-4079	Sequence 4079, Ap
	38	7	1.2	712	3	US-08-998-416-687	Sequence 687, App
	39	7	1.2	717	4	US-09-328-352-887	Sequence 887, App
c	40	7	1.2	723	4	US-09-252-991A-5872	Sequence 5872, Ap
	41	7	1.2	726	4	US-09-328-352-3875	Sequence 3875, Ap
c	42	7	1.2	747	4	US-09-328-352-2394	Sequence 2394, Ap
	43	7	1.2	750	4	US-09-134-001C-2741	Sequence 2741, Ap
	44	7	1.2	750	4	US-09-328-352-1368	Sequence 1368, Ap
	45	7	1.2	867	4	US-09-252-991A-13395	Sequence 13395, A